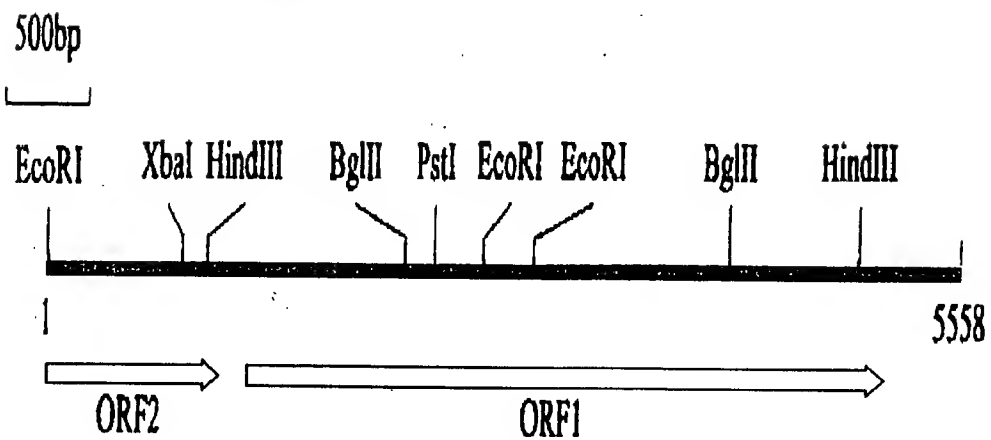


Fig 1



a)

PCR

b)

inverse PCR

c)

EcoRI BglII EcoRI HindIII
clone 1 clone 2

d)

PCR

inverse PCR

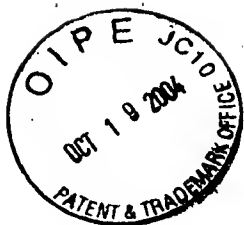
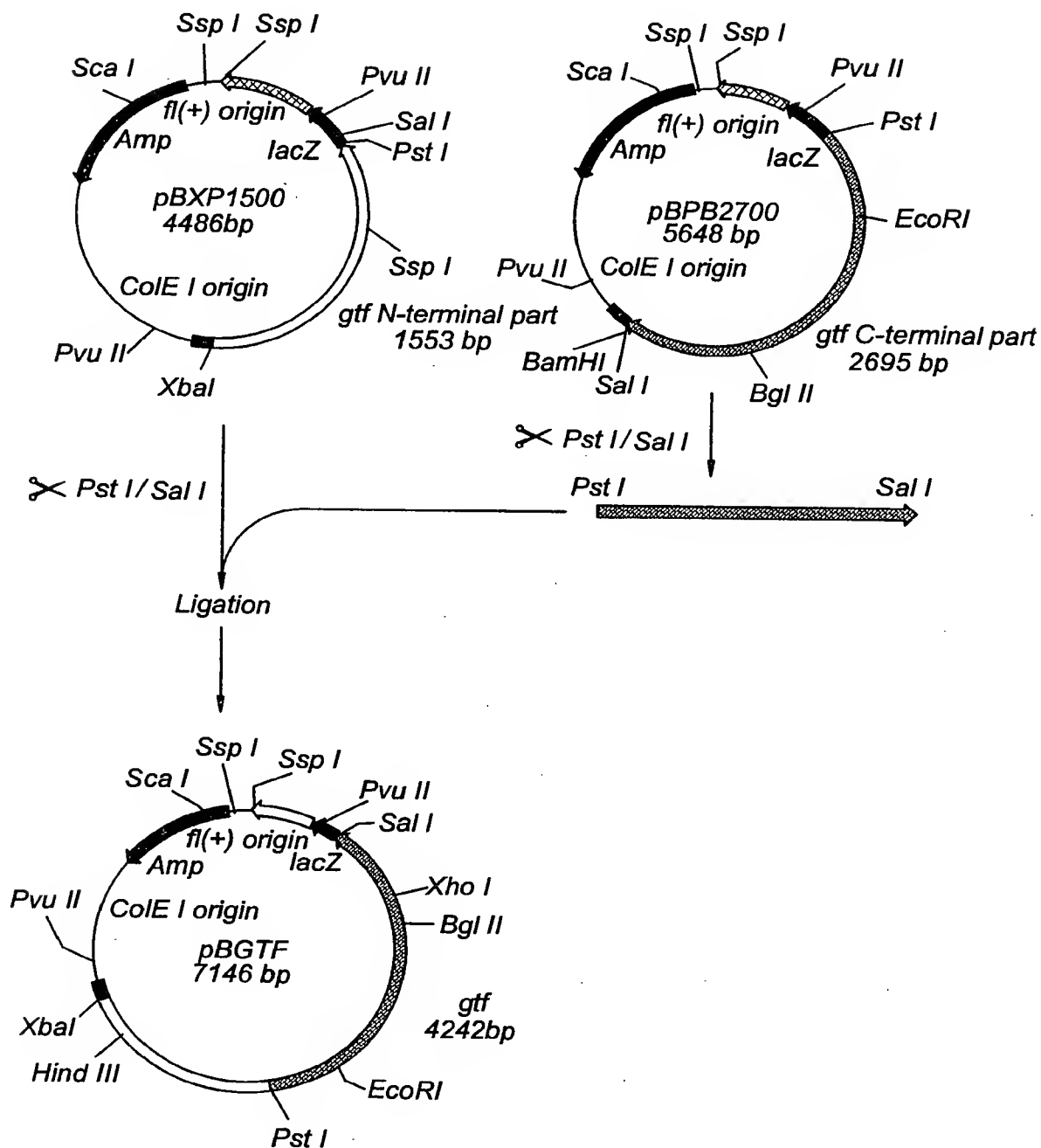


Fig 2



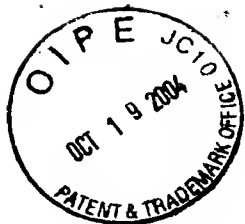


Fig. 3.1

◇ ↓ ∇∇

GTFD	LLANDIDNSNPVVQAEQLNWLHYLMNYGSIVANDPEANFDGVRVDAVDNVNADLLQIASD	480
DSRS	LLANDVDNSNVVVEAEQLNWLYYLMNFGTITANDADANFDGIRVDAVDNVADLLQIAAD	576
ASR	LLANDIDNSNPVQAEQLNWLHYLMNFGSITGNNDNANFDGIRVDAVDNVADLLKIAGD	650
GTFA	LLANDIDNSNPVVQAEQLNWLYYLLNFGTITANNDQANFDSVRVDA <u>PDN</u> <u>IDADLM</u> <u>NIAQD</u>	509
	***** . ***** * . * . * * * * * . ***** ** . *** . * * *	
AS	262QWDLN ₂₆₆	.290IVRMDAVAFI ₂₉₈
	-----H3-----	--E4- -----H4--
	↓∇∇∇	
GTFD	YLKAHYGVDKSEKNAINHLSILEAWSNDNPQYNKDTKGAQLPIDNKLRLSLLYALTRPLE	540
DSRS	YFKLAYGVDQNDATANQHLSILEDWSHNDPLYVTDQGSNQLTMDDYVHTQLIWSLTK--S	634
ASR	YFKALYGTDKSDANANKHLSILEDWNGKDPQYVNRQQGNAQLTMDYTVTSQFGNSLTHGAN	710
GTFA	YFNAAYGMD-SDAVSNKHINILEDWNHADPEYFNKIGNPQLTMDDTIK----NSLNHGLS	564
	* * * . . * . * * * * * * * . . * . .	
	-----E5--	---H5---- ---E6--
GTFD	KDASNKNEIRSGLEPVITNSLN-----NRS AEGKNSERMANYIFIRA	582
DSRS	---SD---IRGTMQRFVDYYMV-----DRSNDSTENEAI PNYSFVRA	660
ASR	N-RSN----MWYFLDTGYLLNGDLNKKIVDKNRPN SGTLVNRIANS GDTKVIPNYSFVRA	765
GTFA	D-ATN----RWGLDAIVHQS-----LADRENNSTENVVIPNYSFVRA	601
		* . * * * . *
AS		396FVRS
	-----H6-----	--E7--

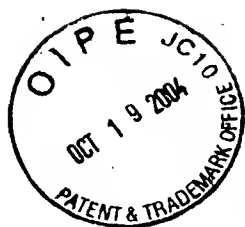


Fig. 3.2



GTFD HDSEVQTVIAKIIKAQINPKTDGLTFTLDELKQAFKIYNEDM--RQAKKKYTQSNIPTAY 640
DSRS HDSEVQTVIAQIVSDLYPDVENS LAPTTEQLAAAFKVYNEDE--KLADKKYTQYNMASAY 718
ASR HDYDAQDP IRKAMIDHGIIKNMQDTFTFDQLAQGMEFYKQDENPSGFKKYNDYNLPSAY 825
GTFA HDNNSQDQIQNAIRDVTGKD--YHTFTFEDEQKGIDAYIQDQ-N-STVKKYNLYNIPASY 657
* * * * *

AS HD₄₀₁

----H7-

GTFD ALMLSNKDSITRLYYGDMYSDDGQYMATKSPYYDAIDTLLKARIKYAAGGQDMKITVEG 700
DSRS AMLLTNKDTPRVYYGDLYTDDGQYMATKSPYYDAINTLLKARVQYVAGGQ----- 769
ASR AMLLTNKDTPRVYYGDMYLEGGQYMEKGTIYNPVISALLKARIKYVSGGQTMATDSSGK 885
GTFA AILLTNKDTIPRVYYGDLYTDDGQYMEHQTRYD⁴⁹⁶TLLNLLKSRVKYVAGGQSMQTM⁴⁹⁶SVG- 716
* . . * . . * . * . . * . * . . * . * . . * . * . . *

AS ⁴⁸⁸GLPRIYLG⁴⁹⁶D

H7-

--E8-

-----H8-----

GTFD DKSHMDWDYTGVLT SVRYGTGANEATDQGSEATK----TQGMVITSNNPSLKLNQNDKV 756
DSRS ---SMSVDSNDVLT SVRYGKDAMTASDTGTSETR----TEGIGVIVSNNAELOLEDGHTV 822
ASR DL---KDGETDLLTSVRFGKGIMTSDQTTTQDNSQDYKNQGIGVIVGNNPDLKLNDKTI 942
GTFA -----GNNNILT SVRYGKGAMTATDTGTDETR----TQGIGVVVSNTPNLKLGVNDKV 765
* . . * . . * . * . . * . * . . * . * . . *

GTFD IVNMGAAHKNQEYRPLLLTTKDGLTSYTSDAAAKSLYRKTND-----K-GELVFD 805
DSRS TLHMGAAHKNQAYRALLSTTADGLAYYDTDENAPVAYTDAN-----GD LIFT 869
ASR TLHMGKAHKNQLYRALVLSNDSGIDVYDSDDKAPT LRTNDNGDLIFHKTNTFVKQDGTII 1002
GTFA VLHMGAAHKNQYRAAVLTTTGDVINYTS DQGA PVAMTDENG DLYLSSHNLVVNGK-EEA 824
* . . * . . * . * . . * . * . . *



Fig. 3.3

GTFD ASDIQGYLNPQVSGYLAVWVPVGASDNQDVRVAASNKANATG-QVYESSSALDSQLIYEG 864
DSRS NESIYGVQNPQVSGYLAVWVPVGAQQDQDARTASDTTNTSD-KVFHSNAALDSQVIYEG 928
ASR NYEMKGSNLALISGYLGWVPVGASDSQDARTVATESSSNDGSVFHSNAALDSNVIYEG 1062
GTFA DTAVQGYANPDVSGYLAVWVPVGASDNQDARTAPSTEKNSGN-SAYRTNAAFDSNVIFEA 883
* * .***** ** * . . . * ** . * . *
-E1-

GTFD FSNFQDFVTKDSYTNKKIAQNVQLFKSWGVTSEMAPQYVSSDGE-----SFLDSIIQN 919
DSRS FSNFQAFATDSSEYTNVIAQNAQDQFKQWGVTSFQLAPQYRSSTDTE-----SFLDSIIQN 983
ASR FSNFQAMPTSPEQSTNVVIATKANLEKELGITSFELAPQYRSSGDTNYGGMSFLDSFLNN 1122
GTFA FSNFVYTPTKESERANVRIAQNADEFFASLGFTSFEMAPQYNSSKDR-----TELDSTIDN 938
**** * . * ** * * * * . * * * * . * * * *

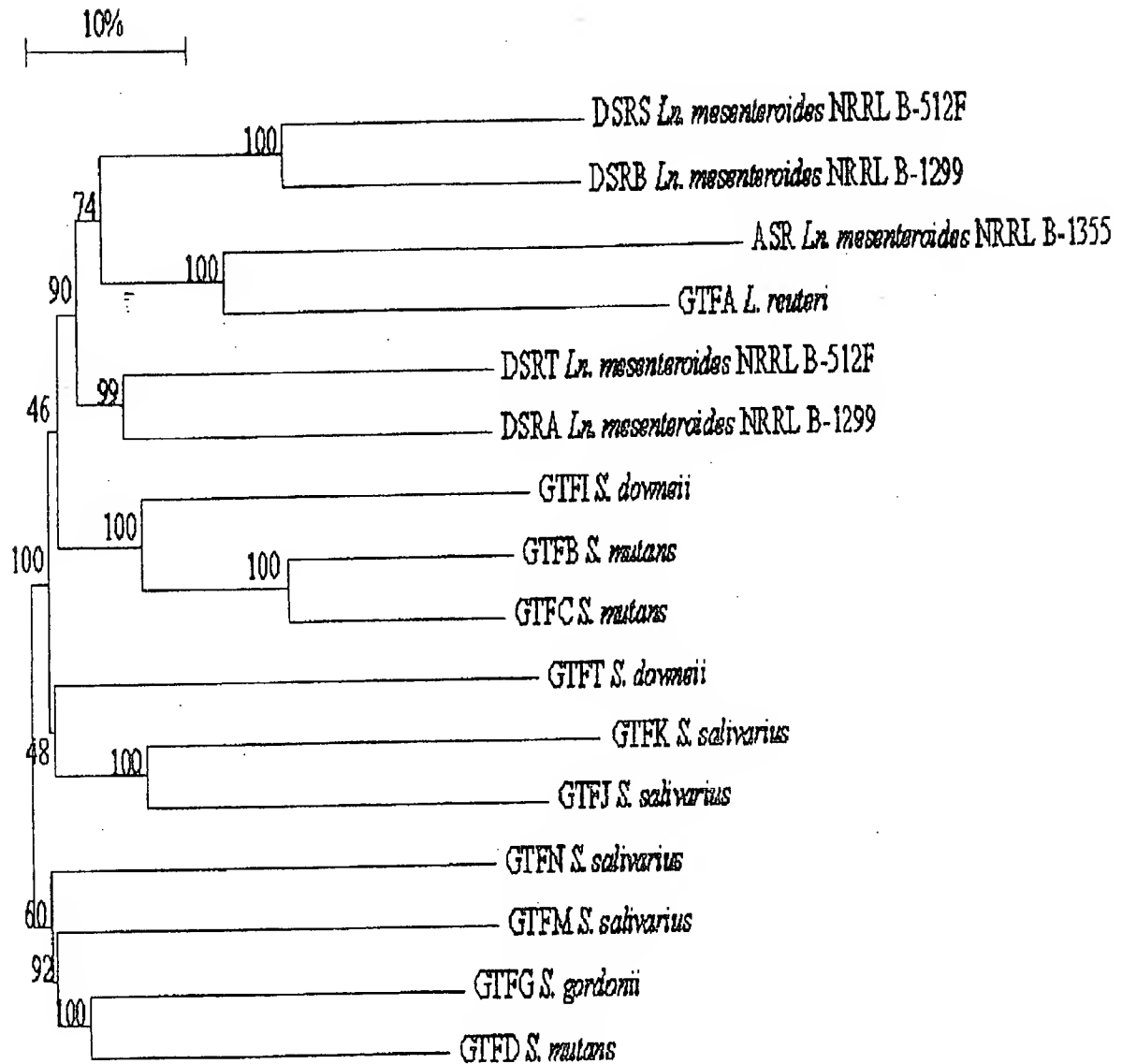
AS 134GLTYLHLMF142
---H1--- --E2-

GTFD GYAFEDRYDLAMSKN--N----KYGSQQDMINAVKALHKSGIQVIADWVPDQ 965
DSRS GYAFTDRYDLGYGTP--T----KYGTADQLRDAIKALHASGIQAIADWVPDQ 1029
ASR GYAFTDRYDLGFNKADGNPNPTKYGTDQDLRNAIEALHKNGMQAIADWVPDQ 1174
GTFA GYAFTDRYDLGMSEP--N----KYGTDEDLRNAIQALHKAGLQVMADWVPDQ 984
**** * * * * . * * * * . * * * * * . * * * * *

AS 190DFITNH195
-----H2----- ---E3--



Fig. 4



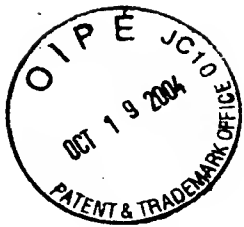


Fig. 4.1

◇ ↓ ∇∇

GTFD	LLANDIDNSNPVVQAEQLNWLHYLMNYGSIVANDPEANFDGVRVDAVDNVNADLLQIASD	480
DSRS	LLANDVDNSNVVVEAEQLNWLYYLMNFGTITANDADANFDGIRVDAVDNVDADLLQIAAD	576
ASR	LLANDIDNSNPVQAEQLNWLHYLMNFGSITGNNDNANFDGIRVDAVDNVDADLLKIAGD	650
GTFD	LLANDIDNSNPVVQAEQLNWLYYLLNFGTITANNDQANFDSVRVDAVDNVDADLLMNIQD	509
***** . ***** . * . * . * . * . * . * . * . * . * . * . * . *		
AS	²⁶² QWDLN ₂₆₆	²⁹⁰ IVRMDAVAFI ₂₉₈
	-----H3-----	--E4- -----H4--
↓∇∇∇		
GTFD	YLKAHYGVDKSEKNAINHLSILEAWSNDPQYNKDTKGAQLPIDNKLRLSLLYALTRPLE	540
DSRS	YFKLAYGVDQNDATANQHLSILEDWSHNDPLYVTDQGSNQLTMDDYVHTQLIWSLTK--S	634
ASR	YFKALYGTDKSDANANKHLSILEDWNGKDPQYVNQQNAQLTMDYTVTSQFGNSLTHGAN	710
GTFD	YFNAAYGMD-SDAVSNKHINILEDWNHADPEYFNKIGNPQLTMDDTIK----NSLNHGLS	564
* * * * . . * . * * * * * * * * . * . * . .		
	-----E5--	---H5--- -----E6--
GTFD	KDASNKNEIRSGLEPVITNSLN-----NRS AEGKNSERMANYIFIRA	582
DSRS	---SD---IRGTMQREFVDYYMV-----DRSNDSTENEAI PNYSFVRA	660
ASR	N-RSN---MWFYLD TGY YLNGDLNKKIVDKNRPN SGT LVNRIANS GDTKVIPNYSFVRA	765
GTFD	D-ATN---RWGLDAIVHQS-----LADRENNSTENVVIPNYSFVRA	601
* . * * * . * *		
AS		³⁹⁶ FVRS
	-----H6-----	--E7--

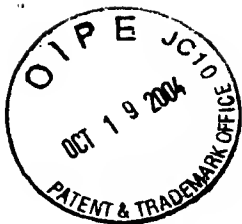


Fig. 4.2



GTFD HDSEVQTVIAKIIKAQINPKTDGLTFTLDELKQAFKIYNEDM--RQAKKKYTQSNIP TAY 640
DSRS HDSEVQTVIAQIVSDLYPDVENS LAPTEQLAAAFKVYNEDE--KLADKKYTQYNMASAY 718
ASR HDYDAQDPIRKAMIDHGI IKNMQDTFTFDQLAQGMEFYKQENPSGFKKYNDYNLPSAY 825
GTFA HDNNSQDQIQNAIRDVTGKD--YHTFTFEDEQKGIDAYIQDQ-N-STVKKYNLYNIPASY 657
* * * * *

AS HD₄₀₁

----H7-

GTFD ALMLSNKDSITRLYYGDMYSDDGQYMATKSPYYDAIDTLLKARIKYAAGGQDMKITYVEG 700
DSRS AMLLTNKDTVPRVYYGDLYTDDGQYMATKSPYYDAINTLLKARVQYVAGGQ----- 769
ASR AMLLTNKDTVPRVYYGDMYLEGGQYMEKGTIYNPVISALLKARIKYVSGGQTMATDSSGK 885
GTFA AILLTNKDTIPRVYYGDLYTDGGQYMEHQTRYD⁴⁹⁶TLNLLKSRVKYVAGGQSMQTMSVG- 716
* . . . * . . . * . . . * . . . * . . . * . . . *

AS ⁴⁸⁸GLPRIYLGD₄₉₆

H7-

--E8-

-----H8-----

GTFD DKSHMDWDYTGVLTSVRYGTGANEATDQGSEATK----TQGMVITSNNPSLKLNQNDKV 756
DSRS ---SMSVDSNDVLTSVRYGKDAMTASDTGTSETR----TEGIGVIVSNNAELOLEDGHTV 822
ASR DL---KDGETDLLTSVREGKGIMTSDQTTTQDNSQDYKNQGIGVIVGNNPDLKLNNDKTI 942
GTFA -----GNNNILTSVRYGKGAMTATDTGTDETR----TQGIGVVVSNTPNLKLGVNDKV 765
* . . . * . . . * . . . * . . . *

GTFD IVNMGAAHKNQEYRPLLLTTKDG⁴⁹⁶LSYTSDA⁴⁹⁶AKSLYRKTND-----K-GELVFD 805
DSRS TLHMGAAHKNQAYRALLSTTADGLAYYDTDENAPVAYTDAN-----GD⁴⁹⁶LIFT 869
ASR TLHMGKAHKNQLYRALVLSNDSGIDVYDSDDKAPTLRTNDNGDLIFHKTNTFVKQDGTII 1002
GTFA VLHMGAAHKNQYRAAVLTTT⁴⁹⁶DGVINYTS⁴⁹⁶DQ⁴⁹⁶GAPVAMTDENG⁴⁹⁶DLYLSSHNLVVNGK-EEA 824
* . . . * . . . * . . . *



Fig.4.3

GTFD ASDIQGYLNPQVSGYLAVWVPVGASDNQDVRVAASNKANATG-QVYESSSALDSQLIYEG 864
DSRS NESIYGVQNPQVSGYLAVWVPVGAQQDQDARTASDTTNTSD-KVFHSNAALDSQVIYEG 928
ASR NYEMKGSNLALISGYLGWVPVGASDSQDARTVATESSSSNDGSVFHSNAALDSNVIYEG 1062
GTFA DTAVQGYANPDVSGYLAVWVPVGASDNQDARTAPSTEKNSGN-SAYRTNAAFDSNVIFEA 883

. * * . ***** * * * . . . * * . . . *

-E1-

GTFD FSNEQDFVTKDSDYTNKKIAQNVQLFKSWGVTSEMAPQYVSSSEDG-----SFLDSIIQN 919
DSRS FSNEQAFATDSSEYTNVIAQNAQDFKQWGVTSFQLAPQYRSSTDt-----SFLDSIIQN 983
ASR FSNEQAMPTSPEQSTNVVIATKANLFKELGITSFELAPQYRSSGDTNYGGMSFLDSFLNN 1122
GTFA FSNEVYTPTKESERANVRIAQNAFFASLGFTSFEMAPQYNSSKDR-----TFLDSTIDN 938

**** * . * ** * * * * . ***** * * . ***** . *

AS

134GLTYLHLM_{P142}

---H1--

--E2-

GTFD GYAFEDRYDLAMSKN--N----KYGSQQDMINAVKALHKSGIQVIADWVPDQ 965
DSRS GYAFTDRYDLGYGTP--T----KYGTADQLRDAIKALHASGIQAIADWVPDQ 1029
ASR GYAFTDRYDLGFNKADGNPNPTKYGTDQDLRNAIEALHKNGMQAIADWVPDQ 1174
GTFA GYAFTDRYDLGMSEP--N----KYGTDEDLRNAIQALHKAGLQVMADWVPDQ 984

***** * . * * * . * . * * * . * . * * * . *

AS

190DFITNH₁₉₅

-----H2----- ---E3--



Fig.5

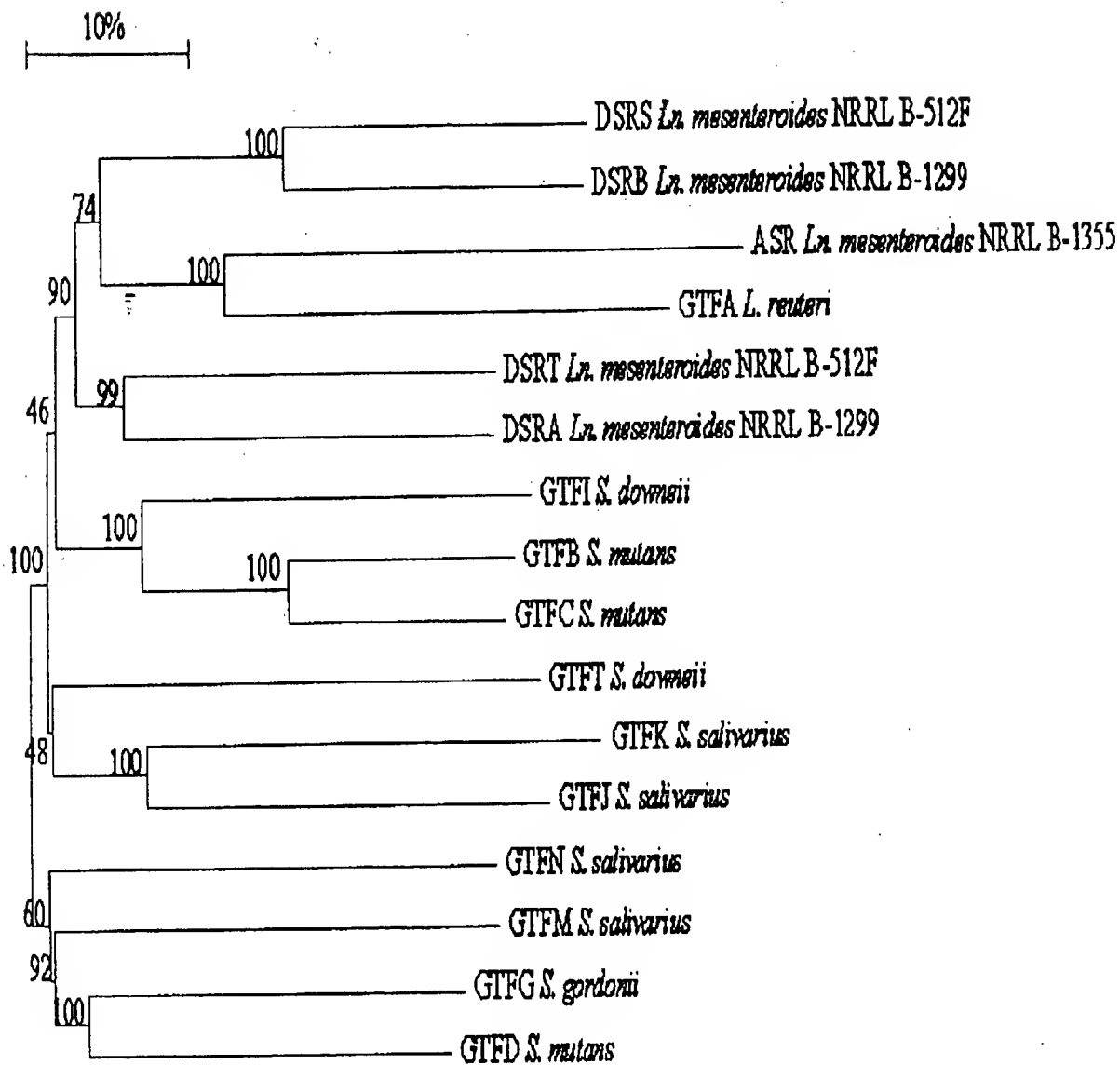
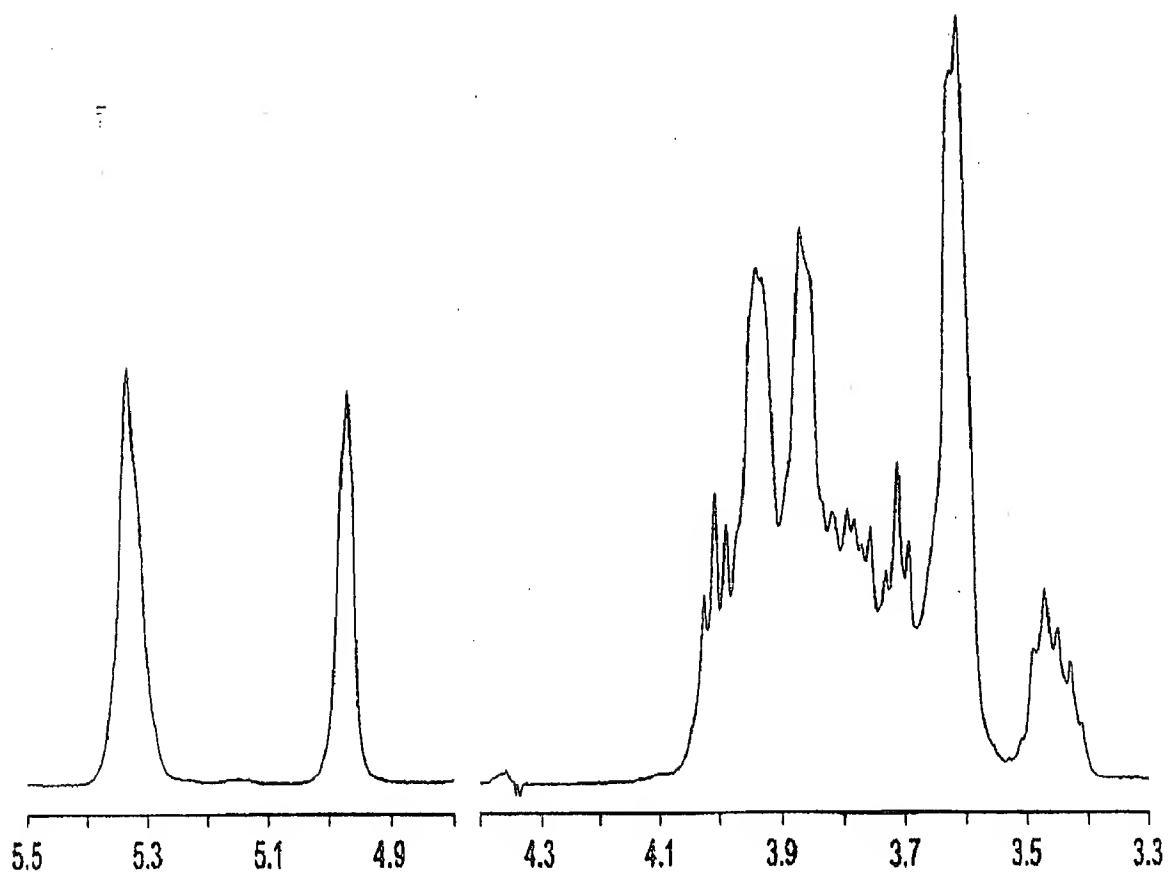




Fig. 5a



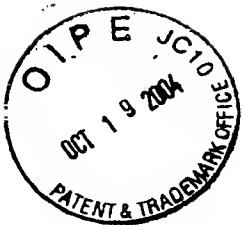


Fig. 5b

